

SEQUENCE LISTING

<110> Levy, Stuart, et. al.

<120> NIMR COMPOSITIONS AND THEIR METHODS OF USE

<130> PKZ-043.

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<150> 60/188,362

<151> 2000-03-10

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<170> PatentIn Ver. 2.0

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agc Ser 835	cgt Arg	gag Glu	aac Asn	ctg Leu	cgt Arg	cac His 840	cac His	ttc Phe	gaa Glu	gtt Val	gat Asp 845	gct Ala	tct Ser	tat Tyr	gtc Val	7943
gtg Gly	gtt Gly	gcg Gly	gcg Gly	ctg Gly	ggc Gly	gaa Gly	ctg Gly	gct Gly	aaa Gly	cgt Gly	ggc Gly	gaa Gly	atc Gly	gat Gly	aag Gly	7991

gaa gca ggc gcg gca gct ccg gcc gct aaa cag gaa gca gct ccg gca 8665
Glu Ala Gly Ala Ala Ala Pro Ala Ala Lys Gln Glu Ala Ala Pro Ala

1070	1075	1080	1085	
gcg gcc cct gca cca gcg gct ggc gtg aaa gaa gtt aac gtt ccg gat				8713
Ala Ala Pro Ala Pro Ala Ala Gly Val Lys Glu Val Asn Val Pro Asp				
	1090	1095	1100	
atc ggc ggt gac gaa gtt gaa gtg act gaa gtg atg gtg aaa gtg ggc				8761
Ile Gly Gly Asp Glu Val Glu Val Thr Glu Val Met Val Lys Val Gly				
	1105	1110	1115	
gac aaa gtt gcc gct gaa cag tca ctg atc acc gta gaa ggc gac aaa				8809
Asp Lys Val Ala Ala Glu Gln Ser Leu Ile Thr Val Glu Gly Asp Lys				
	1120	1125	1130	
gct tct atg gaa gtt ccg gcg ccg ttt gca ggc gtc gtg aag gaa ctg				8857
Ala Ser Met Glu Val Pro Ala Pro Phe Ala Gly Val Val Lys Glu Leu				
	1135	1140	1145	
aaa gtc aac gtt ggc gat aaa gtg aaa act ggc tcg ctg att atg atc				8905
Lys Val Asn Val Gly Asp Lys Val Lys Thr Gly Ser Leu Ile Met Ile				
	1150	1155	1160	1165
ttc gaa gtt gaa ggc gca gcg cct gcg gca gct cct gcg aaa cag gaa				8953
Phe Glu Val Glu Gly Ala Ala Pro Ala Ala Ala Pro Ala Lys Gln Glu				
	1170	1175	1180	
gcg gca gcg ccg gca ccg gca gca aaa gct gaa gcc ccg gca gca gca				9001
Ala Ala Ala Pro Ala Pro Ala Ala Lys Ala Glu Ala Pro Ala Ala Ala				
	1185	1190	1195	
cca gct gcg aaa gcg gaa ggc aaa tct gaa ttt gct gaa aac gac gct				9049
Pro Ala Ala Lys Ala Glu Gly Lys Ser Glu Phe Ala Glu Asn Asp Ala				
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tat gtt cac gcg act ccg ctg atc cgc cgt ctg gca cgc gag ttt ggt				9097
Tyr Val His Ala Thr Pro Leu Ile Arg Arg Leu Ala Arg Glu Phe Gly				
	1215	1220	1225	
gtt aac ctt gcg aaa gtg aag ggc act ggc cgt aaa ggt cgt atc ctg				9145
Val Asn Leu Ala Lys Val Lys Gly Thr Gly Arg Lys Gly Arg Ile Leu				
	1230	1235	1240	1245
cgc gaa gac gtt cag gct tac gtg aaa gaa gct atc aaa cgt gca gaa				9193
Arg Glu Asp Val Gln Ala Tyr Val Lys Glu Ala Ile Lys Arg Ala Glu				
	1250	1255	1260	
gca gct ccg gca gcg act ggc ggt ggt atc cct ggc atg ctg ccg tgg				9241
Ala Ala Pro Ala Ala Thr Gly Gly Gly Ile Pro Gly Met Leu Pro Trp				
	1265	1270	1275	
ccg aag gtg gac ttc agc aag ttt ggt gaa atc gaa gaa gtg gaa ctg				9289
Pro Lys Val Asp Phe Ser Lys Phe Gly Glu Ile Glu Glu Val Glu Leu				
	1280	1285	1290	
ggc cgc atc cag aaa atc tct ggt gcg aac ctg agc cgt aac tgg gta				9337
Gly Arg Ile Gln Lys Ile Ser Gly Ala Asn Leu Ser Arg Asn Trp Val				
	1295	1300	1305	

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Met Ile Pro His Val Thr His Phe Asp Lys Thr Asp Ile Thr Glu Leu
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gaa gcg ttc cgt aaa cag cag aac gaa gaa gcg gcg aaa cgt aag ctg 9433
Glu Ala Phe Arg Lys Gln Gln Asn Glu Glu Ala Ala Lys Arg Lys Leu
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gat gtg aag atc acc ccg gtt gtc ttc atc atg aaa gcc gtt gct gca 9481
Asp Val Lys Ile Thr Pro Val Val Phe Ile Met Lys Ala Val Ala Ala
1345 1350 1355

gct ctt gag cag atg cct cgc ttc aat agt tcg ctg tcg gaa gac ggt 9529
Ala Leu Glu Gln Met Pro Arg Phe Asn Ser Ser Leu Ser Glu Asp Gly
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cag cgt ctg acc ctg aag aaa tac atc aac atc ggt gtg gcg gtg gat 9577
Gln Arg Leu Thr Leu Lys Lys Tyr Ile Asn Ile Gly Val Ala Val Asp
1375 1380 1385

acc ccg aac ggt ctg gtt gtt ccg gta ttc aaa gac gtc aac aag aaa 9625
Thr Pro Asn Gly Leu Val Val Pro Val Phe Lys Asp Val Asn Lys Lys
1390 1395 1400 1405

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Arg Asp Gly Lys Leu Thr Ala Gly Glu Met Gln Gly Gly Cys Phe Thr
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Asn Ala Pro Glu Val Ala Ile Leu Gly Val Ser Lys Ser Ala Met Glu
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Pro Val Trp Asn Gly Lys Glu Phe Val Pro Arg Leu Met Leu Pro Ile
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Ser Leu Ser Phe Asp His Arg Val Ile Asp Gly Ala Asp Gly Ala Arg
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10157

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<213> Escherichia coli

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Val Asn Val Ala Ala Gly Thr Gly Ile Ser Asn Tyr Ile Asn Thr Ile
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Pro Val Glu Glu Gln Pro Glu Tyr Pro Gly Asn Leu Glu Leu Glu Arg
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Arg Ile Arg Ser Ala Ile Arg Trp Asn Ala Ile Met Thr Val Leu Arg
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Ala Ser Lys Lys Asp Leu Glu Leu Gly Gly His Met Ala Ser Phe Gln
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Ser Ser Ala Thr Ile Tyr Asp Val Cys Phe Asn His Phe Phe Arg Ala
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Arg Asn Glu Gln Asp Gly Gly Asp Leu Val Tyr Phe Gln Gly His Ile
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Ser Pro Gly Val Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Gln
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Glu Gln Leu Asp Asn Phe Arg Gln Glu Val His Gly Asn Gly Leu Ser
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Ser Tyr Pro His Pro Lys Leu Met Pro Glu Phe Trp Gln Phe Pro Thr
180 185 190

Val Ser Met Gly Leu Gly Pro Ile Gly Ala Ile Tyr Gln Ala Lys Phe
195 200 205

Leu Lys Tyr Leu Glu His Arg Gly Leu Lys Asp Thr Ser Lys Gln Thr
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Val Tyr Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Lys
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Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Thr Gly Asn
260 265 270

Gly Lys Ile Ile Asn Glu Leu Glu Gly Ile Phe Glu Gly Ala Gly Trp
275 280 285

Asn Val Ile Lys Val Met Trp Gly Ser Arg Trp Asp Glu Leu Leu Arg
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Lys Asp Thr Ser Gly Lys Leu Ile Gln Leu Met Asn Glu Thr Val Asp
305 310 315 320

Gly Asp Tyr Gln Thr Phe Lys Ser Lys Asp Gly Ala Tyr Val Arg Glu
325 330 335

His Phe Phe Gly Lys Tyr Pro Glu Thr Ala Ala Leu Val Ala Asp Trp
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Thr Asp Glu Gln Ile Trp Ala Leu Asn Arg Gly Gly His Asp Pro Lys
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Lys Ile Tyr Ala Ala Phe Lys Lys Ala Gln Glu Thr Lys Gly Lys Ala
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Ala Glu Gly Lys Asn Ile Ala His Gln Val Lys Lys Met Asn Met Asp
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Gly Val Arg His Ile Arg Asp Arg Phe Asn Val Pro Val Ser Asp Ala
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Asp Ile Glu Lys Leu Pro Tyr Ile Thr Phe Pro Glu Gly Ser Glu Glu
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His Thr Tyr Leu His Ala Gln Arg Gln Lys Leu His Gly Tyr Leu Pro
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Asp Phe Gly Ala Leu Leu Glu Glu Gln Ser Lys Glu Ile Ser Thr Thr
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Lys Asp Arg Leu Val Pro Ile Ile Ala Asp Glu Ala Arg Thr Phe Gly
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Met Glu Gly Leu Phe Arg Gln Ile Gly Ile Tyr Ser Pro Asn Gly Gln
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Gln Tyr Thr Pro Gln Asp Arg Glu Gln Val Ala Tyr Tyr Lys Glu Asp
545 550 555 560

Glu Lys Gly Gln Ile Leu Gln Glu Gly Ile Asn Glu Leu Gly Ala Gly
565 570 575

Cys Ser Trp Leu Ala Ala Ala Thr Ser Tyr Ser Thr Asn Asn Leu Pro
580 585 590

Met Ile Pro Phe Tyr Ile Tyr Tyr Ser Met Phe Gly Phe Gln Arg Ile
595 600 605

Gly Asp Leu Cys Trp Ala Ala Gly Asp Gln Gln Ala Arg Gly Phe Leu
610 615 620

Ile Gly Gly Thr Ser Gly Arg Thr Thr Leu Asn Gly Glu Gly Leu Gln
625 630 635 640

His Glu Asp Gly His Ser His Ile Gln Ser Leu Thr Ile Pro Asn Cys
645 650 655

Ile Ser Tyr Asp Pro Ala Tyr Ala Tyr Glu Val Ala Val Ile Met His
660 665 670

Asp Gly Leu Glu Arg Met Tyr Gly Glu Lys Gln Glu Asn Val Tyr Tyr
675 680 685

Tyr Ile Thr Thr Leu Asn Glu Asn Tyr His Met Pro Ala Met Pro Glu
690 695 700

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Glu Gly Ser Lys Gly Lys Val Gln Leu Leu Gly Ser Gly Ser Ile Leu
725 730 735

Arg His Val Arg Glu Ala Ala Glu Ile Leu Ala Lys Asp Tyr Gly Val
740 745 750

Gly Ser Asp Val Tyr Ser Val Thr Ser Phe Thr Glu Leu Ala Arg Asp
755 760 765

Gly Gln Asp Cys Glu Arg Trp Asn Met Leu His Pro Leu Glu Thr Pro
770 775 780

Arg Val Pro Tyr Ile Ala Gln Val Met Asn Asp Ala Pro Ala Val Ala
785 790 795 800

Ser Thr Asp Tyr Met Lys Leu Phe Ala Glu Gln Val Arg Thr Tyr Val
805 810 815

Pro Ala Asp Asp Tyr Arg Val Leu Gly Thr Asp Gly Phe Gly Arg Ser
820 825 830

Asp Ser Arg Glu Asn Leu Arg His His Phe Glu Val Asp Ala Ser Tyr
835 840 845

Val Val Val Ala Ala Leu Gly Glu Leu Ala Lys Arg Gly Glu Ile Asp
850 855 860

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35 40 45

Ser Pro Gln Ala Gly Ile Val Lys Glu Ile Lys Val Ser Val Gly Asp
50 55 60

Lys Thr Gln Thr Gly Ala Leu Ile Met Ile Phe Asp Ser Ala Asp Gly
65 70 75

Ala Ala Asp Ala Ala Pro Ala Gln Ala Glu Glu Lys Lys Glu Ala Ala
80 85 90 95

Pro Ala Ala Ala Pro Ala Ala Ala Ala Lys Asp Val Asn Val Pro
100 105 110

Asp Ile Gly Ser Asp Glu Val Glu Val Thr Glu Ile Leu Val Lys Val
115 120 125

Gly Asp Lys Val Glu Ala Glu Gln Ser Leu Ile Thr Val Glu Gly Asp
130 135 140

Lys Ala Ser Met Glu Val Pro Ala Pro Phe Ala Gly Thr Val Lys Glu
145 150 155

Ile Lys Val Asn Val Gly Asp Lys Val Ser Thr Gly Ser Leu Ile Met
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Val Phe Glu Val Ala Gly Glu Ala Gly Ala Ala Pro Ala Ala Lys
180 185 190

Gln Glu Ala Ala Pro Ala Ala Ala Pro Ala Pro Ala Ala Gly Val Lys
195 200 205

Glu Val Asn Val Pro Asp Ile Gly Gly Asp Glu Val Glu Val Thr Glu
210 215 220

Val Met Val Lys Val Gly Asp Lys Val Ala Ala Glu Gln Ser Leu Ile
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 Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val Pro Ala Pro Phe Ala
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 Gly Val Val Lys Glu Leu Lys Val Asn Val Gly Asp Lys Val Lys Thr
 260 265 270
 Gly Ser Leu Ile Met Ile Phe Glu Val Glu Gly Ala Ala Pro Ala Ala
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 Ala Pro Ala Lys Gln Glu Ala Ala Ala Pro Ala Pro Ala Ala Lys Ala
 290 295 300
 Glu Ala Pro Ala Ala Ala Pro Ala Ala Lys Ala Glu Gly Lys Ser Glu
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 Phe Ala Glu Asn Asp Ala Tyr Val His Ala Thr Pro Leu Ile Arg Arg
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 Arg Lys Gly Arg Ile Leu Arg Glu Asp Val Gln Ala Tyr Val Lys Glu
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 Ile Gly Val Ala Val Asp Thr Pro Asn Gly Leu Val Val Pro Val Phe
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 Lys Asp Val Asn Lys Lys Gly Ile Ile Glu Leu Ser Arg Glu Leu Met
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Thr Ile Ser Lys Lys Ala Arg Asp Gly Lys Leu Thr Ala Gly Glu Met
530 535 540

Gln Gly Gly Cys Phe Thr Ile Ser Ser Ile Gly Gly Leu Gly Thr Thr
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His Phe Ala Pro Ile Val Asn Ala Pro Glu Val Ala Ile Leu Gly Val
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Ser Lys Ser Ala Met Glu Pro Val Trp Asn Gly Lys Glu Phe Val Pro
580 585 590

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Arg Gly Val Val Lys His Leu Gln Leu Arg Asn Asn Ser Phe Gly Gly
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Val Asp Met Val Ile Ser Gly Asn Val Pro Gln Gly Ala Gly Leu Ser
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Ser Ser Ala Ser Leu Glu Val Ala Val Gly Thr Val Leu Gln Gln Leu
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Tyr His Leu Pro Leu Asp Gly Ala Gln Ile Ala Leu Asn Gly Gln Glu
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Ala Glu Asn Gln Phe Val Gly Cys Asn Cys Gly Ile Met Asp Gln Leu
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Lys Asn Pro Asp Tyr Thr Gly Thr Tyr Val Phe Thr Asn Asp Phe Ala
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Ala Leu Met Ser Asp Thr Pro Asp Ala Pro Glu Ser His Asp Pro Leu
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Met Arg Cys Gln Ser Ala Arg Gly Thr Ser Arg Val Ile Cys Phe Ser
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Pro Asp His Ser Lys Thr Leu Pro Glu Leu Ser Val Ala Ala Leu Thr
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Glu Ile Val Lys Thr Trp Gln Glu Gln Thr Ala Glu Leu Gly Lys Thr
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Tyr Pro Trp Val Gln Val Phe Glu Asn Lys Gly Ala Ala Met Gly Cys
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Ser Asn Pro His Pro His Gly Gln Ile Trp Ala Asn Ser Phe Leu Pro
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Asn Glu Ala Glu Arg Glu Asp Arg Leu Gln Lys Glu Tyr Phe Ala Glu
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Gln Lys Ser Pro Met Leu Val Asp Tyr Val Gln Arg Glu Leu Ala Asp
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Gly Ser Arg Thr Val Val Glu Thr Glu His Trp Leu Ala Val Val Pro
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Tyr Trp Ala Ala Trp Pro Phe Glu Thr Leu Leu Leu Pro Lys Ala His

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Tyr Asp His Leu Gly Lys Arg Thr Ser Leu Pro Gly Ser Thr Gly Leu	110	115	120	
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Asn Ala Thr Gly Pro Trp Val Lys Gln Phe Phe Asp Asp Gly Met His	205	210	215	
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atc aat cca acg cag acc gct gcc tgg cag gca cta cag aaa cac ttc 525

Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln Lys His Phe

5

10

15

gat gaa atg aaa gac gtt acg atc gcc gat ctt ttt gct aaa gac ggc 573

Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala Lys Asp Gly

20

25

30

35

gat cgt ttt tct aag ttc tcc gca acc ttc gac gat cag atg ctg gtg 621

Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln Met Leu Val

40

45

50

gat tac tcc aaa aac cgc atc act gaa gag acg ctg gcg aaa tta cag 669

Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala Lys Leu Gln

55

60

65

gat ctg gcg aaa gag tgc gat ctg gcg ggc gcg att aag tcg atg ttc 717

Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys Ser Met Phe

70

75

80

tct ggc gag aag atc aac cgc act gaa aac cgc gcc gtg ctg cac gta 765

Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val Leu His Val

85

90

95

gcg ctg cgt aac cgt agc aat acc ccg att ttg gtt gat ggc aaa gac 813

Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp Gly Lys Asp

100

105

110

115

gta atg ccg gaa gtc aac gcg gtg ctg gag aag atg aaa acc ttc tca 861

Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys Thr Phe Ser

120

125

130

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Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly Asn Met Glu	
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1. The first step is to identify the problem. This involves understanding the symptoms and the context in which they are occurring.

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1. The first part of the report is a general introduction to the project, which includes a brief history of the organization and a statement of its mission.

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 Pro Asp Val Pro Arg Tyr Thr Glu Glu Tyr Arg Lys His Leu Val Glu
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Gln Glu Tyr Ile Lys Glu Ala Gln Gly Cys Asp Ile Arg Cys Leu Val

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1. The first part of the report is a general statement of the purpose of the study.

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Met Asn Ile Leu His Ile Cys

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Val Thr Ser Lys Trp Phe Asn Ile Asp Asn Lys Ile Val Asp His Arg

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Pro

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 Asp Glu Gln Leu Ala Glu Tyr Tyr Leu Thr Arg Gly Ser Asn Asn Arg
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Questions are asked whether there is any connection between the two cases.